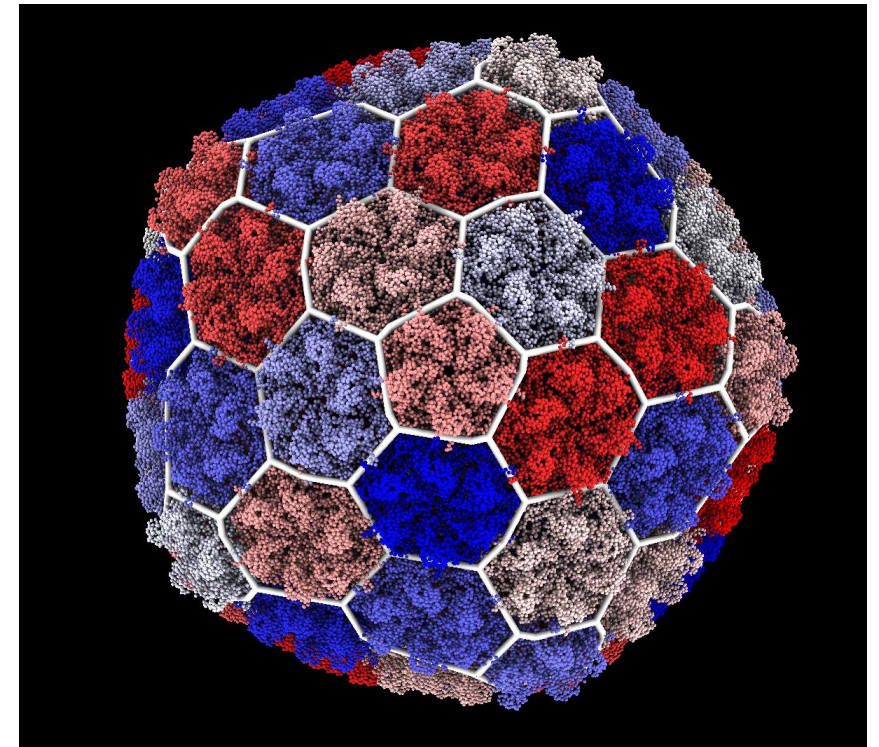
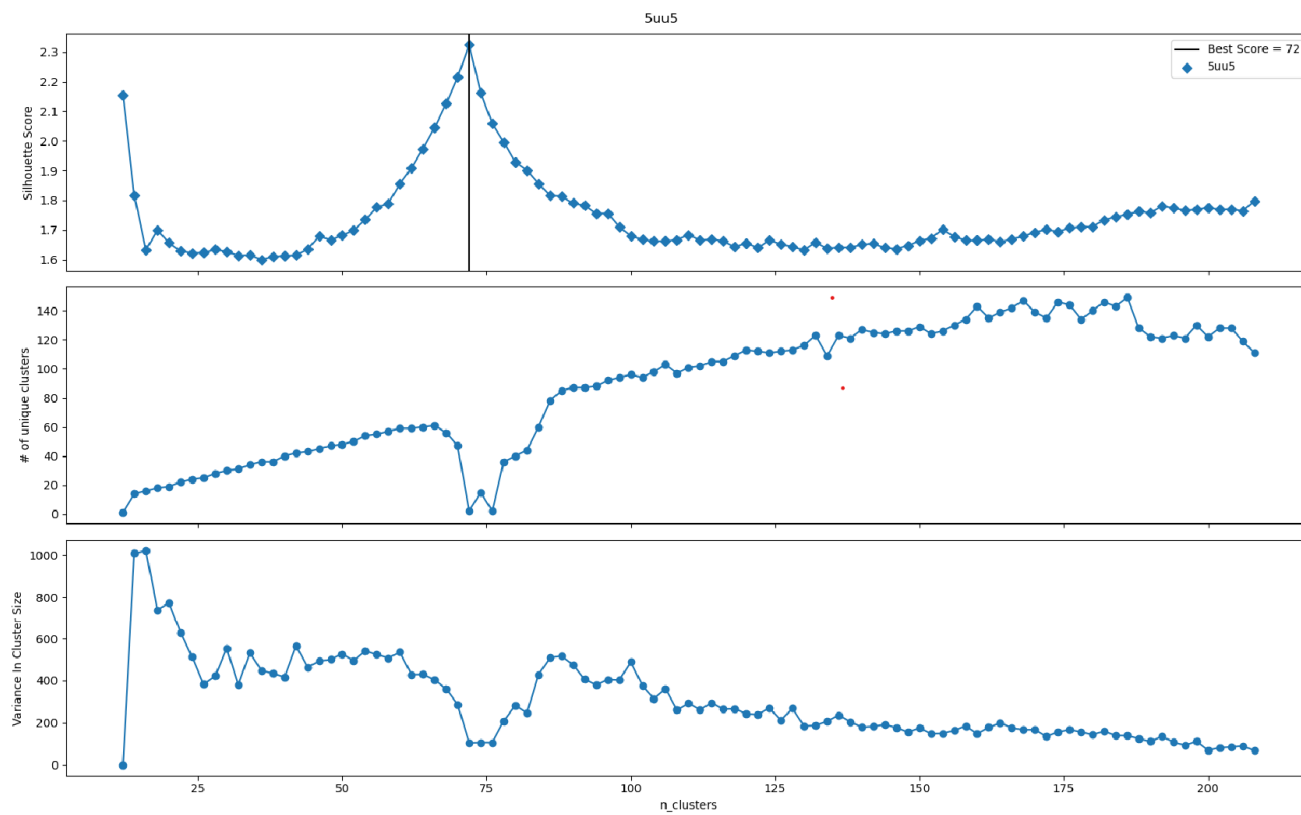


HK97 Results

Results

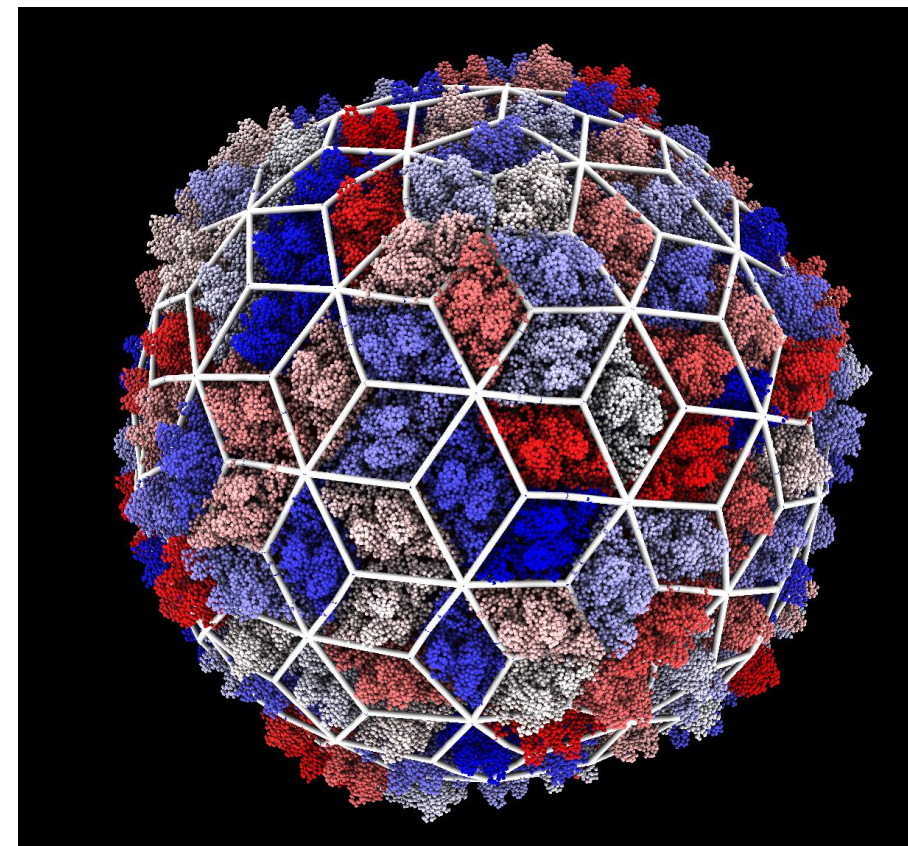
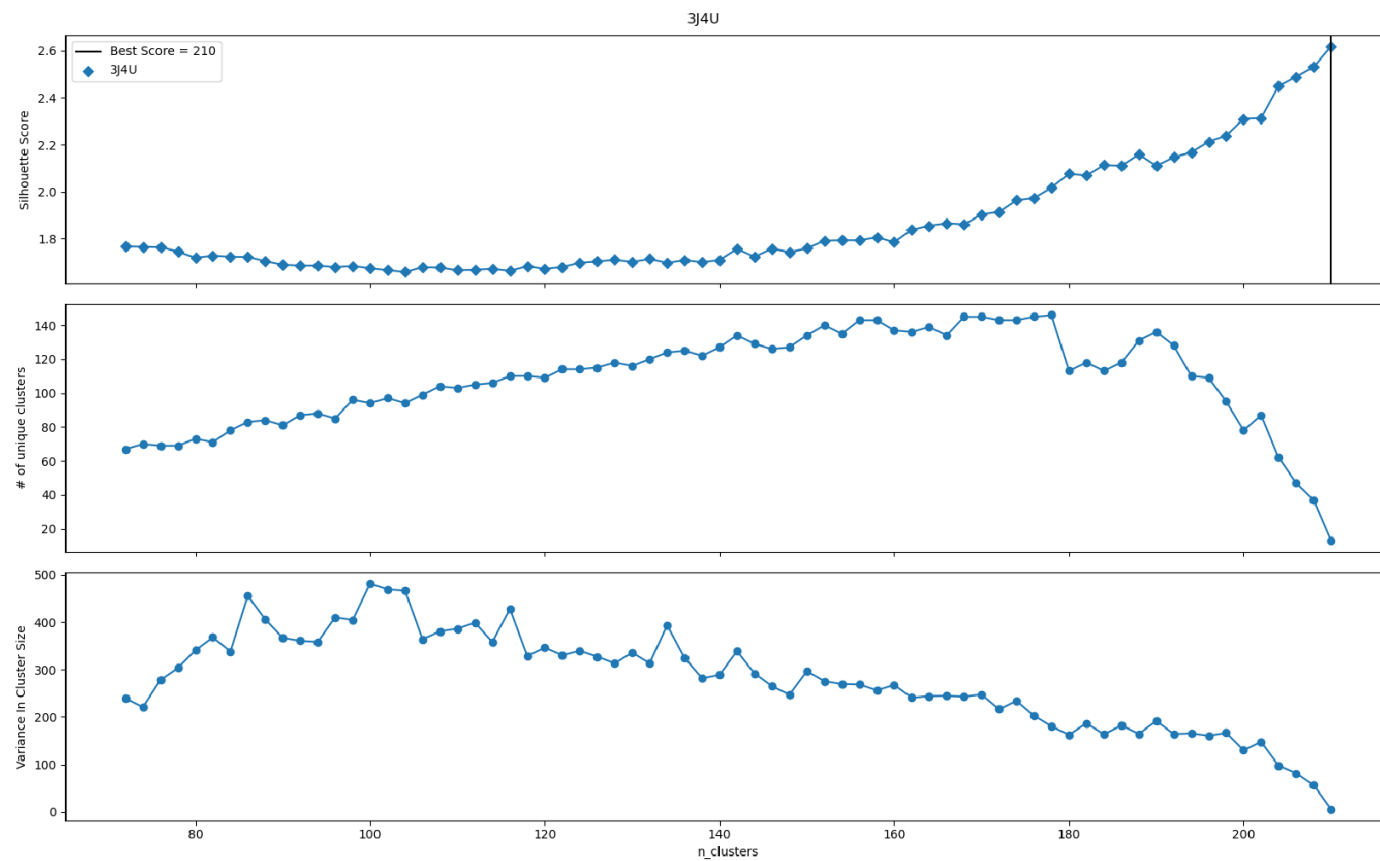
- ▶ T=7 Architectures
 - ▶ 5uu5 - Hexagonal
 - ▶ 6xgq – Trihex
 - ▶ 3j4u – Trihex

P22 Mature – 5UU5



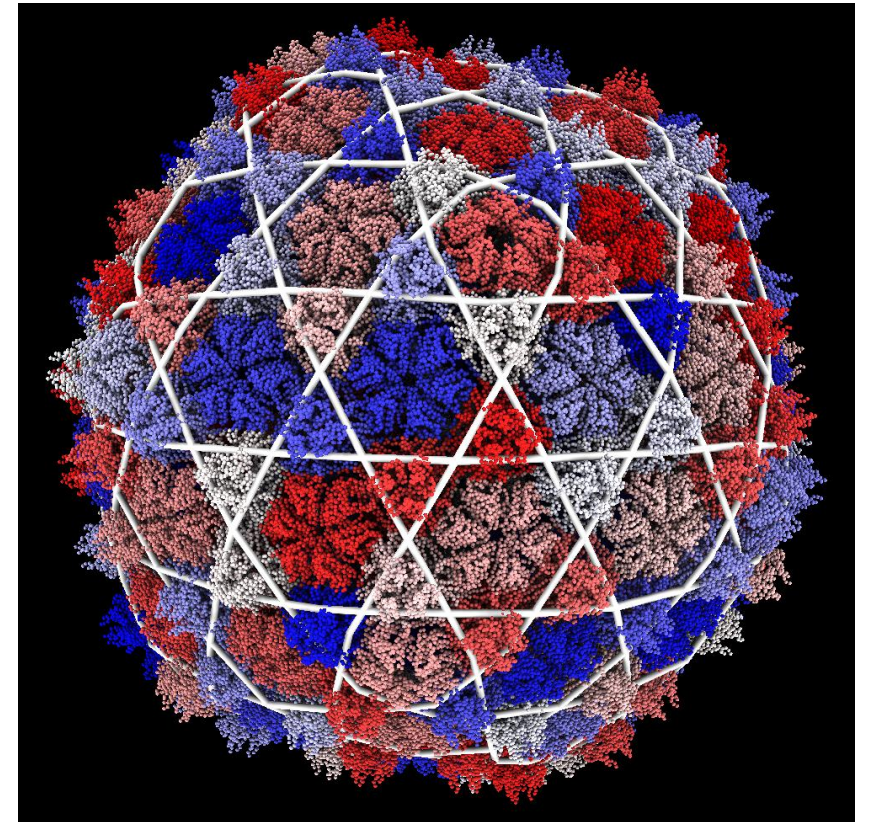
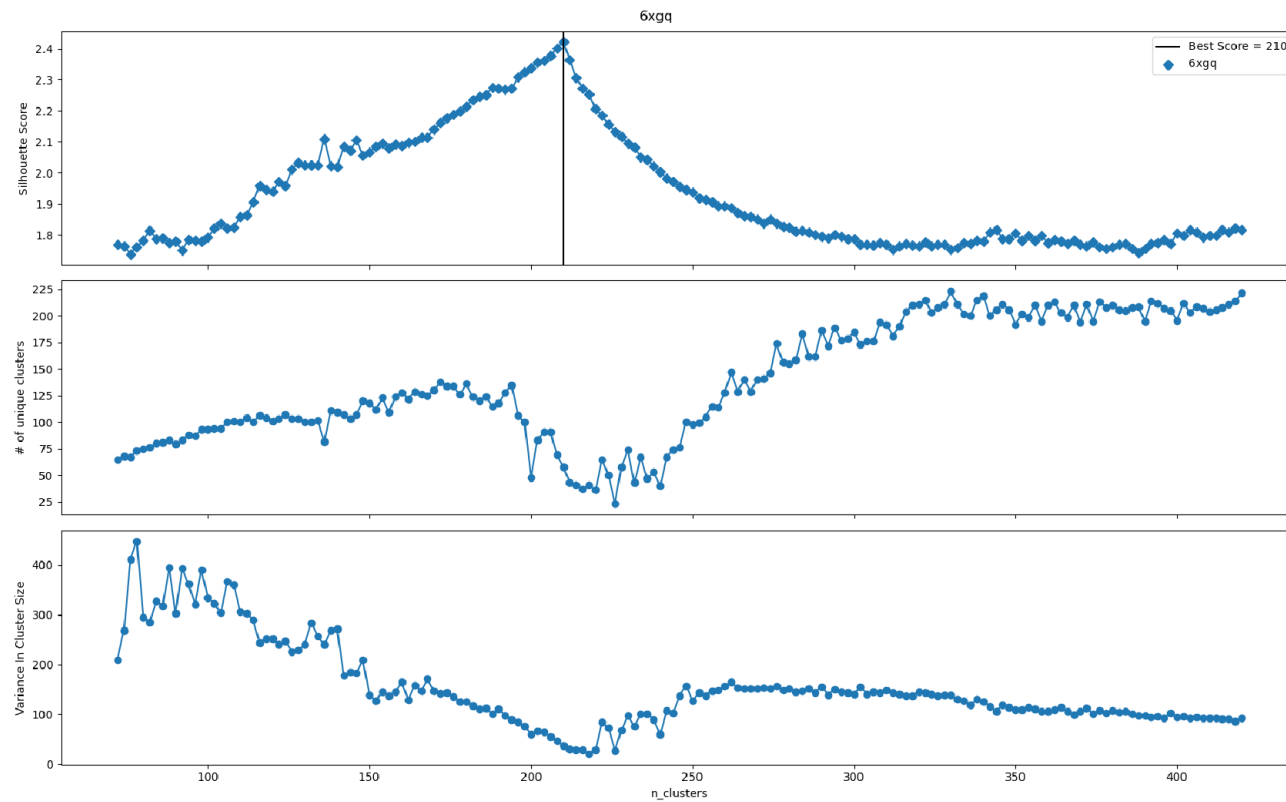
3J4U – Bordetella Bacteriophage

Imperfect



6xgq - YSD1 Bacteriophage

Imperfect



Discussion

- ▶ P22 lacked reinforcement proteins and was labelled as hexagonal
- ▶ Bordetella and Phage YSD1 had reinforcement proteins around the local 2-fold and 3-fold axes respectively and were labeled as trihex-dual and trihex.
- ▶ This suggests the presence and location of reinforcement proteins could determine lattice structure.
- ▶ Both Bordatella and YSD1 had error in their label assignments. The tool becomes less accurate at a large number of clusters.